Artem Lysenko

List of Publications by Year in descending order

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759233 713466 22 743 12 21 h-index citations g-index papers 24 24 24 1147 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Transcriptome and Metabolite Profiling of the Infection Cycle of <i>Zymoseptoria tritici</i> on Wheat Reveals a Biphasic Interaction with Plant Immunity Involving Differential Pathogen Chromosomal Contributions and a Variation on the Hemibiotrophic Lifestyle Definition Â. Plant Physiology, 2015, 167, 1158-1185.	4.8	301
2	Representing and querying disease networks using graph databases. BioData Mining, 2016, 9, 23.	4.0	75
3	Developing integrated crop knowledge networks to advance candidate gene discovery. Applied & Translational Genomics, 2016, 11, 18-26.	2.1	66
4	An integrative machine learning approach for prediction of toxicity-related drug safety. Life Science Alliance, 2018, 1, e201800098.	2.8	44
5	Genetical and Comparative Genomics of <i>Brassica</i> under Altered Ca Supply Identifies <i>Arabidopsis</i> Ca-Transporter Orthologs Â. Plant Cell, 2014, 26, 2818-2830.	6.6	40
6	DeepFeature: feature selection in nonimage data using convolutional neural network. Briefings in Bioinformatics, 2021, 22, .	6.5	31
7	A novel approach to identify genes that determine grain protein deviation in cereals. Plant Biotechnology Journal, 2015, 13, 625-635.	8.3	28
8	Recon2Neo4j: applying graph database technologies for managing comprehensive genome-scale networks. Bioinformatics, 2017, 33, 1096-1098.	4.1	25
9	Data integration for plant genomics-exemplars from the integration of Arabidopsis thaliana databases. Briefings in Bioinformatics, 2009, 10, 676-693.	6.5	21
10	Network-Based Data Integration for Selecting Candidate Virulence Associated Proteins in the Cereal Infecting Fungus Fusarium graminearum. PLoS ONE, 2013, 8, e67926.	2.5	18
11	EpiGeNet: A Graph Database of Interdependencies Between Genetic and Epigenetic Events in Colorectal Cancer. Journal of Computational Biology, 2017, 24, 969-980.	1.6	16
12	Navigating the disease landscape: knowledge representations for contextualizing molecular signatures. Briefings in Bioinformatics, 2019, 20, 609-623.	6.5	16
13	Assessing the functional coherence of modules found in multiple-evidence networks from Arabidopsis. BMC Bioinformatics, 2011, 12, 203.	2.6	14
14	AIGO: Towards a unified framework for the Analysis and the Inter-comparison of GO functional annotations. BMC Bioinformatics, 2011, 12, 431.	2.6	12
15	Discovering Study-Specific Gene Regulatory Networks. PLoS ONE, 2014, 9, e106524.	2.5	8
16	PHI-Nets: A Network Resource for Ascomycete Fungal Pathogens to Annotate and Identify Putative Virulence Interacting Proteins and siRNA Targets. Frontiers in Microbiology, 2019, 10, 2721.	3.5	8
17	Detection of Multi-clustered Genes and Community Structure for the Plant Pathogenic Fungus Fusarium graminearum. Lecture Notes in Computer Science, 2012, , 69-86.	1.3	8
18	Interactive exploration of integrated biological datasets using context-sensitive workflows. Frontiers in Genetics, 2014, 5, 21.	2.3	4

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#	Article	IF	CITATIONS
19	Immune subtypes and neoantigen-related immune evasion in advanced colorectal cancer. IScience, 2022, 25, 103740.	4.1	4
20	Analysis and visualisation of RDF resources in Ondex. Nature Precedings, 2010, , .	0.1	1
21	Integrating Multiple Studies of Wheat Microarray Data to Identify Treatment-Specific Regulatory Networks. Lecture Notes in Computer Science, 2013, , 104-115.	1.3	1
22	A Framework for Mining Life Sciences Data on the Semantic Web in an Interactive, Graph-Based Environment. Lecture Notes in Computer Science, 2014, , 225-237.	1.3	0